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JUN 26 2001

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> McKeon, F.  
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<120> CALCIPRESSINS: ENDOGENOUS INHIBITORS OF CALCINEURIN  
USES AND REAGENTS RELATED THERETO

<130> HMSU-P01-048

<140> 09/575,580

<141> 2000-05-22

<160> 45

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe	35	40	45
Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala	50	55	60
Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu	65	70	75
Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu	85	90	95
Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser	100	105	110
Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn	115	120	125
Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr	130	135	140
Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val	145	150	155
Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg	165	170	175
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Thr Pro Ile His Leu Ser	195		

<210> 5  
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Arg Asp Trp Ala Val Thr Gln Cys Phe Ala Glu Glu Ala Phe Gln Ala
35 40 45
Leu Thr Asp Phe Ser Asp Leu Pro Asn Ser Leu Phe Ala Cys Asn Val
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His	Gln	Ser	Val	Phe	Glu	Glu	Glu	Glu	Ser	Lys	Glu	Lys	Phe	Glu	Gly
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Leu	Phe	Arg	Thr	Tyr	Asp	Glu	Cys	Val	Thr	Phe	Gln	Leu	Phe	Lys	Ser
				85					90					95	
Phe	Arg	Arg	Val	Arg	Ile	Asn	Phe	Ser	His	Pro	Lys	Ser	Ala	Ala	Arg
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Ala	Arg	Ile	Glu	Leu	His	Glu	Thr	Gln	Phe	Arg	Gly	Lys	Lys	Leu	Pro
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Leu	Tyr	Phe	Ala	Gln	Val	Gln	Thr	Pro	Glu	Thr	Asp	Gly	Asp	Lys	Leu
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His	Leu	Ala	Pro	Pro	Gln	Pro	Ala	Lys	Gln	Phe	Leu	Ile	Ser	Pro	Pro
145					150				155						160
Ser	Ser	Pro	Ser	Val	Gly	Trp	Lys	Pro	Ile	Ser	Asp	Ala	Thr	Pro	Val
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Leu	Asn	Tyr	Asp	Leu	Leu	Tyr	Ala	Val	Ala	Lys	Leu	Gly	Pro	Gly	Glu
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 <213> Homo sapiens

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Thr	Tyr	Asp	Asp	Cys	Val	Thr	Phe	Gln	Leu	Phe	Lys	Ser	Phe	Arg	Arg
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Val	Arg	Ile	Asn	Phe	Ser	Asn	Pro	Lys	Ser	Ala	Ala	Arg	Ala	Arg	Ile
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 Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro  
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 Pro Val Gly Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr  
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 Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu  
 130 135 140  
 Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys  
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<210> 7

<211> 170

<212> PRT

<213> Homo sapiens

<400> 7

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Ser Asn Pro Phe Ser Ala Ala Asp Ala Arg Leu Gln Leu His Lys Thr  
 35 40 45

Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu His  
 50 55 60

Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu  
 65 70 75 80

Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu Asp  
 85 90 95

Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu  
 100 105 110

Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr Pro  
 115 120 125

Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu

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 Glu Glu Met Glu Arg Met Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr  
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Arg Arg Pro Glu Tyr Thr Pro Ile His Leu  
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<210> 8  
 <211> 197  
 <212> PRT  
 <213> Cricetulus griseus

<400> 8  
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Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe  
 35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala  
 50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu  
 65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu  
 85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser  
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Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn  
 115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr  
 130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val  
 145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Met Glu Arg Met  
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Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr  
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Pro Ile His Leu Ser  
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<210> 9  
 <211> 207

<212> PRT

<213> *Caenorhabditis elegans*

<400> 9

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35 40 45  
Ala Asn Phe Ser Ser Leu Phe Thr Gln Ile Glu Lys Asp Ile His Phe  
50 55 60  
Asp Phe Leu Arg Ser Phe Arg Arg Val Arg Val Ile Phe Ser Ser Pro  
65 70 75 80  
Glu Asn Ala Thr Ala Ala Lys Leu Ile Val Gln Gly Phe Ser Phe Lys  
85 90 95  
Gly His Glu Leu Lys Ala Phe Phe Ala Gln Arg Ile Tyr Met Ser Ala  
100 105 110  
Asn Ser Gln Met Leu Ser Pro Pro Pro Leu Glu Lys Gln Phe Leu Ile  
115 120 125  
Ser Pro Pro Cys Ser Pro Pro Val Gly Trp Glu Gln Thr Lys Asp Met  
130 135 140  
Pro Pro Val Val Cys Asn Phe Asp Leu Met Ala Arg Leu Ala Ser Phe  
145 150 155 160  
Ala Ile Asp Glu Lys Tyr Glu Val His Asn Gly Asp Glu Leu Thr Pro  
165 170 175  
Ala Ile Ile Val His Pro Cys Glu Thr Pro Ile Asp Val Pro Ser Ala  
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Ile Glu Met Pro Arg Thr Pro Arg Pro Ser Ser Pro Cys Glu Gln  
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<210> 10

<211> 211

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 10

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Lys Asn Ile Leu Arg Lys Phe Gln Ile Asn Glu Asn Glu Pro Leu Gln

35	40	45
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50	55	60
His Asp Ile Ser Gln His Val Met Asp Ala Ser Arg Ala Leu Glu Met		
65	70	75
		80
Glu Asn Phe Asn Phe Ser Tyr Ser Leu Gln Asp Gly Gln Arg Asn Leu		
	85	90
		95
Thr Lys Gln Tyr Leu Lys Val Pro Glu Ser Glu Lys Met Phe Leu Ile		
	100	105
		110
Ser Pro Pro Ala Ser Pro Pro Pro Glu Phe Asp Phe Ser Lys Cys Glu		
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		125
Asp Ala Pro Gln Arg His Ile Gln Ser His Ile Gln Gln Asp Gln Gln		
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Gln Arg Leu Glu Ala Ser Gln Leu Leu Pro Asn Asn Pro Asp Lys Asn		
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Ile Asp Arg Cys Pro Thr Asn Asp Gly Asn Gly Gln Met Gln Leu Ala		
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 <213> Schizosaccharomyces pombe

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Thr Leu Lys Lys Ser Ser Thr Gly Ser Leu Pro Ser Gly Gln Gln Val
50 55 60
His Cys Gln Tyr Val Leu Asp Asp Pro Asn His Val Glu Gly Ile Ser
65 70 75 80



Val Asp Gln Ser Leu Gln Val Pro Lys Phe Glu Lys Asn Trp Leu Ile  
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 Ser Pro Pro Gly Ser Pro Pro Val Gly Trp Glu Pro Ile Val Glu Glu  
 100 105 110  
 Ser Pro Asn Ser Gln His Leu Ala His Asp Ile Gln Leu Lys Leu Asp  
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 Glu Leu Gly Asn Ala Leu Leu Asn Asp His Ser Ala Gly Pro Gln Ile  
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<210> 12  
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 <212> PRT  
 <213> Homo sapiens

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<210> 13  
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<400> 21

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<211> 724

<212> DNA

<213> Mus musculus

<400> 22

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<213> Mus musculus

<400> 24

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Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Val Gln Glu Gln	50	55	60
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Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser Glu Asp Ala	145	150	155
Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser Lys Leu Gly	165	170	175
Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser	180	185	190
Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu Glu Asp Thr	195	200	205
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<210> 27

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<212> DNA

<213> Mus musculus

<220>

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: general structure

<220>

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<223> Xaa=any amino acid residue

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antagonist

<400> 29

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<210> 30

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: calcineurin  
antagonist

<400> 30

Pro Lys Pro Lys Ile Asn Gln Thr Arg Arg Pro Gly  
1 5 10

<210> 31

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: EGF-derived  
peptide

<400> 31

Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys  
1 5 10

<210> 32

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: EGF-derived  
peptide

<400> 32

Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys  
1 5 10

<210> 33

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pH-dependent  
membrane-binding internalizing peptide

<220>  
<221> SITE  
<222> (1)  
<223> Xaa=preferably a unique residue, such as Cys or  
Lys, that facilitates chemical conjugation of the  
internalizing peptide to a targeting protein  
conjugate

<220>  
<221> SITE  
<222> (2)..(3)  
<223> Xaa=residues selected to modulate the affinity of  
the internalizing peptide for different membranes

<400> 33  
Xaa Xaa Xaa Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala  
1 5 10 15  
Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala  
20 25 30

<210> 34  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide  
substrate

<400> 34  
Gly Asn Ala Ala Ala Arg Arg  
1 5

<210> 35  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (4)..(75)

<220>  
<223> Description of Artificial Sequence: synthetic  
construct

<400> 35  
cat atg ggt ggc tgc cgt ggc gat atg ttc ggt tgc ggt gct cct cca 48  
Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro  
1 5 10 15

aaa aag aag aga aag gta gct gga ttc  
 Lys Lys Lys Arg Lys Val Ala Gly Phe  
 20

75

<210> 36

<211> 24

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: synthetic  
 construct

<400> 36

Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro Lys  
 1 5 10 15

Lys Lys Arg Lys Val Ala Gly Phe  
 20

<210> 37

<211> 225

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
 construct

<220>

<221> CDS

<222> (4) .. (225)

<400> 37

cat atg gag cca gta gat cct aga cta gag ccc tgg aag cat cca gga 48  
 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly  
 1 5 10 15

agt cag cct aaa act gct tgt acc aat tgc tat tgt aaa aag tgt tgc 96  
 Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys  
 20 25 30

ttt cat tgc caa gtt tgt ttc ata aca aaa gcc ctt ggc atc tcc tat 144  
 Phe His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr  
 35 40 45

ggc agg aag aag cgg aga cag cga cga aga cct cct caa ggc agt cag 192  
 Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln  
 50 55 60

act cat caa gtt tct cta agt aag caa gga ttc 225  
 Thr His Gln Val Ser Leu Ser Lys Gln Gly Phe  
 65 70

<210> 38  
 <211> 74  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: synthetic  
 construct

<400> 38  
 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser  
 1 5 10 15  
 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe  
 20 25 30  
 His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly  
 35 40 45  
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr  
 50 55 60  
 His Gln Val Ser Leu Ser Lys Gln Gly Phe  
 65 70

<210> 39  
 <211> 912  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: synthetic  
 construct

<220>  
 <221> CDS  
 <222> (4)..(912)

<400> 39  
 cat atg acc tct cgc cgc tcc gtg aag tcg ggt ccg cgg gag gtt ccg 48  
 Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro  
 1 5 10 15  
 cgc gat gag tac gag gat ctg tac tac acc ccg tct tca ggt atg gcg 96  
 Arg Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala  
 20 25 30  
 agt ccc gat agt ccg cct gac acc tcc cgc cgt ggc gcc cta cag aca 144  
 Ser Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr  
 35 40 45  
 cgc tcg cgc cag agg ggc gag gtc cgt ttc gtc cag tac gac gag tcg 192  
 Arg Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser  
 50 55 60  
 gat tat gcc ctc tac ggg ggc tcg tca tcc gaa gac gac gaa cac ccg 240  
 Asp Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro

65	70	75	
gag gtc ccc cgg acg cgg cgt ccc gtt tcc ggg gcg gtt ttg tcc ggc			288
Glu Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly			
80	85	90	95
ccg ggg cct gcg cgg gcg cct ccg cca ccc gct ggg tcc gga ggg gcc			336
Pro Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala			
	100	105	110
gga cgc aca ccc acc acc gcc ccc cgg gcc ccc cga acc cag cgg gtg			384
Gly Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gln Arg Val			
	115	120	125
gcg act aag gcc ccc gcg gcc ccg ggg gcg gag acc acc cgc ggc agg			432
Ala Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg			
	130	135	140
aaa tcg gcc cag cca gaa tcc gcc gca ctc cca gac gcc ccc gcg tcg			480
Lys Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser			
	145	150	155
acg gcg cca acc cga tcc aag aca ccc gcg cag ggg ctg gcc aga aag			528
Thr Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys			
	160	165	170
ctg cac ttt agc acc gcc ccc cca aac ccc gac gcg cca tgg acc ccc			576
Leu His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro			
	180	185	190
cgg gtg gcc ggc ttt aac aag cgc gtc ttc tgc gcc gcg gtc ggg cgc			624
Arg Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg			
	195	200	205
ctg gcg gcc atg cat gcc cgg atg gcg gcg gtc cag ctc tgg gac atg			672
Leu Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met			
	210	215	220
tcg cgt ccg cgc aca gac gaa gac ctc aac gaa ctc ctt ggc atc acc			720
Ser Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr			
	225	230	235
acc atc cgc gtg acg gtc tgc gag ggc aaa aac ctg ctt cag cgc gcc			768
Thr Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala			
	240	245	250
aac gag ttg gtg aat cca gac gtg gtg cag gac gtc gac gcg gcc acg			816
Asn Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr			
	260	265	270
gcg act cga ggg cgt tct gcg gcg tcg cgc ccc acc gag cga cct cga			864
Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg			
	275	280	285
gcc cca gcc cgc tcc gct tct cgc ccc aga cgg ccc gtc gag gaa ttc			912
Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu Glu Phe			

290

295

300

&lt;210&gt; 40

&lt;211&gt; 303

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;223&gt; Description of Artificial Sequence: synthetic construct

&lt;400&gt; 40

Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro Arg  
 1 5 10 15

Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala Ser  
 20 25 30

Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr Arg  
 35 40 45

Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser Asp  
 50 55 60

Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro Glu  
 65 70 75 80

Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly Pro  
 85 90 95

Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala Gly  
 100 105 110

Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gln Arg Val Ala  
 115 120 125

Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg Lys  
 130 135 140

Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser Thr  
 145 150 155 160

Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys Leu  
 165 170 175

His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro Arg  
 180 185 190

Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg Leu  
 195 200 205

Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met Ser  
 210 215 220

Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr Thr  
 225 230 235 240

Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala Asn

	245		250		255										
Glu	Leu	Val	Asn	Pro	Asp	Val	Val	Gln	Asp	Val	Asp	Ala	Ala	Thr	Ala
			260					265					270		
Thr	Arg	Gly	Arg	Ser	Ala	Ala	Ser	Arg	Pro	Thr	Glu	Arg	Pro	Arg	Ala
		275					280					285			
Pro	Ala	Arg	Ser	Ala	Ser	Arg	Pro	Arg	Arg	Pro	Val	Glu	Glu	Phe	
	290					295					300				

<210> 41  
 <211> 120  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: synthetic construct

<220>  
 <221> CDS  
 <222> (4)..(120)

<400> 41	
cat atg gac gtc gac gcg gcc acg gcg act cga ggg cgt tct gcg gcg	48
Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala	
1 5 10 15	
tcg cgc ccc acc gag cga cct cga gcc cca gcc cgc tcc gct tct cgc	96
Ser Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg	
20 25 30	
ccc aga cgg ccc gtc gag gaa ttc	120
Pro Arg Arg Pro Val Glu Glu Phe	
35	

<210> 42  
 <211> 39  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: synthetic construct

<400> 42	
Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser	
1 5 10 15	
Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro	
20 25 30	
Arg Arg Pro Val Glu Glu Phe	
35	

<210> 43  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 43  
aggaggtgga tctgc

15

<210> 44  
<211> 6  
<212> PRT  
<213> Mus musculus

<400> 44  
Glu Arg Met Arg Arg Pro  
1 5

<210> 45  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: consensus  
sequence

<400> 45  
Glu Arg Met Pro Pro Arg Arg Asp  
1 5

a9  
Cont